



**Figure S1:** Bayesian inferred phylogenetic reconstruction of MerA deduced amino acid sequences. Full-length MerA were truncated by the elimination of NmerA sequences prior to alignments. Nodes are labeled with black, gray, green, yellow circles and no circles indicating > 90, > 80, > 70 and > 60 and < 50 % posterior probability values respectively. Red beaded lines indicate thermophilic lineages; bar indicates 3 substitutions per 10 positions. Sequences of

7 dihydrolipoamide dehydrogenase deduced from *lpdA* homologues in the genomes of  
8 *Magnetospirillum magneticum* AMB-1, *Pseudomonas fluorescens* Pf0-1 and *Thermus*  
9 *thermophilus* HB27 were used as outgroups. The bar on the right illustrate phylum level taxa  
10 identification of corresponding clusters in the tree with captions identifying major clades (alpha,  
11 beta/gamma relate to the Proteobacteria, Actino. to Actinobacteria, D/Th to  
12 Deinococcus/Thermus, and Aqu. to Aquificae).